

## RAW SEQUENCE LISTING

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Application Serial Number: 09/721,114A  
Source: FW 16  
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IFW16

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DATE: 01/06/2005

PATENT APPLICATION: US/09/721,114A

TIME: 16:23:35

Input Set : A:\MAFF1.txt

Output Set: N:\CRF4\01062005\I721114A.raw

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3 <110> APPLICANT: Hirohiko Hirochika
4     Muneo Yamazaki
5     Akio Miyao
7 <120> TITLE OF INVENTION: A novel gene involved in brassinosteroid responses
9 <130> FILE REFERENCE: MAFF-1
11 <140> CURRENT APPLICATION NUMBER: US 09/721,114A
12 <141> CURRENT FILING DATE: 2000-11-22
14 <150> PRIOR APPLICATION NUMBER: JP 2000-149106
15 <151> PRIOR FILING DATE: 2000-05-19
17 <160> NUMBER OF SEQ ID NOS: 5
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 4310
23 <212> TYPE: DNA
24 <213> ORGANISM: Oryza sativa
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (655)..(3828)
30 <400> SEQUENCE: 1
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33 cctgcagtagc tcgcccgcac caccaccgcg ccgcccgcgc cgcccgcgtt ccgagaccca 120
35 ctcgatcggg atccaccgcg gcgcgcccgc gcgcctgcgt cctcttcctt ccccgggagc 180
37 cgaccgacca cgccgaccag tcgatctccc tctccgggcg ccaaccgcgt cttagcttca 240
39 tcgaatccac cgccccaccc cgcatctcct cctcctcctc cgacgacgac gactactact 300
41 agtctttctc aataagcccc cctcccgcgc cccccgcctg aagaagaagc agcagctagc 360
43 tccgggggaga ggtcgacggc gcgcggggtg gatcgcgccc cgccccgcct gcgtcgcggc 420
45 tgtcggagca aacgcaaacc cccaggttg ttctagcgtg tgcagcggct agctgattga 480
47 ttgtcttctg tgatatatcc agagctcgtg ttttgtggtt tgtggtttgt ggtttgtgct 540
49 tggattgttg atgtgcta atcgcgcggtt acaagatcac tgctggattg atattgagtt 600
51 gtgcctcggc tgtgctagct gtgtgttgat tctctcctcg tcgtggtgat cgat atg 657
52                                     Met
53                                     1
55 gag att gtt gca gta gat cag gag gga gct cgt gtt gtt ggg acg aac 705
56 Glu Ile Val Ala Val Asp Gln Glu Gly Ala Arg Val Val Gly Thr Asn
57           5           10           15
59 tgt atg ctt gct cgt ggt gga act ggt gct gta gcg cca gtg ttg gag 753
60 Cys Met Leu Ala Arg Gly Gly Thr Gly Ala Val Ala Pro Val Leu Glu
61           20           25           30
63 ctg aca gcg acg cct cgt cag gat gca gcc gct gaa gct ggt gta gac 801
64 Leu Thr Ala Thr Pro Arg Gln Asp Ala Ala Ala Glu Ala Gly Val Asp
65           35           40           45
67 gaa ccg gca caa cac caa tgc gag cat ttc tcc ata aga ggg tat gtt 849
68 Glu Pro Ala Gln His Gln Cys Glu His Phe Ser Ile Arg Gly Tyr Val

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135 cca tgt gaa gaa gtt gtt ctc aaa aga agc tcc aaa tct aag agg aag 1665
136 Pro Cys Glu Glu Val Val Leu Lys Arg Ser Ser Lys Ser Lys Arg Lys
137          325          330          335
139 acg gat aag aag ttg atg aag aag cag cag cac agc aag aaa cgc act 1713
140 Thr Asp Lys Lys Leu Met Lys Lys Gln Gln His Ser Lys Lys Arg Thr
141          340          345          350
143 gcc cag gct gat gtt tca gat gca aag ctt tgt cgg aga aag cca aaa 1761
144 Ala Gln Ala Asp Val Ser Asp Ala Lys Leu Cys Arg Arg Lys Pro Lys
145          355          360          365
147 aag gtg cgg ctt cta tca gaa att ata aat gct aac cag gtt gag gat 1809
148 Lys Val Arg Leu Leu Ser Glu Ile Ile Asn Ala Asn Gln Val Glu Asp
149 370          375          380          385
151 tct aga agt gac gaa gtt cat cgt gaa aat gcc gct gat ccc tgt gag 1857
152 Ser Arg Ser Asp Glu Val His Arg Glu Asn Ala Ala Asp Pro Cys Glu
153          390          395          400
155 gat gat aga agt acc atc ccg gtc ccg atg gaa gta agc atg gat att 1905
156 Asp Asp Arg Ser Thr Ile Pro Val Pro Met Glu Val Ser Met Asp Ile
157          405          410          415
159 cct gtt agc aac cat aca gtg gga gaa gat ggg tta aaa tca agt aag 1953
160 Pro Val Ser Asn His Thr Val Gly Glu Asp Gly Leu Lys Ser Ser Lys
161          420          425          430
163 aac aag aca aaa cgc aaa tac tct gat gtt gta gat gat gga tca tca 2001
164 Asn Lys Thr Lys Arg Lys Tyr Ser Asp Val Val Asp Asp Gly Ser Ser
165          435          440          445
167 ctt atg aac tgg ctg aat gga aaa aag aaa aga act gga agt gtg cat 2049
168 Leu Met Asn Trp Leu Asn Gly Lys Lys Lys Arg Thr Gly Ser Val His
169 450          455          460          465
171 cac aca gtt gct cat cca gct ggg aat ttg agc aac aaa aaa gtg aca 2097
172 His Thr Val Ala His Pro Ala Gly Asn Leu Ser Asn Lys Lys Val Thr
173          470          475          480
175 ccc act gcg agt act cag cat gat gat gag aat gat act gaa aat ggt 2145
176 Pro Thr Ala Ser Thr Gln His Asp Asp Glu Asn Asp Thr Glu Asn Gly
177          485          490          495
179 ctt gac aca aat atg cat aag aca gat gtc tgt cag cat gta tca gaa 2193
180 Leu Asp Thr Asn Met His Lys Thr Asp Val Cys Gln His Val Ser Glu
181          500          505          510
183 atc tcc aca cag agg tgc tca tca aag ggg aaa aca gcg ggt ttg agt 2241
184 Ile Ser Thr Gln Arg Cys Ser Ser Lys Gly Lys Thr Ala Gly Leu Ser
185          515          520          525
187 aag ggg aaa aca cat tca gct gct agt acc aaa tat ggt ggt gaa agc 2289
188 Lys Gly Lys Thr His Ser Ala Ala Ser Thr Lys Tyr Gly Gly Glu Ser
189 530          535          540          545
191 acc aga aat ggt cag aac ata cat gta ctc agc gca gaa gat caa tgc 2337
192 Thr Arg Asn Gly Gln Asn Ile His Val Leu Ser Ala Glu Asp Gln Cys
193          550          555          560
195 cag atg gaa acc gaa aac tct gtt ctg agt cac tcg gca aag gtt tct 2385
196 Gln Met Glu Thr Glu Asn Ser Val Leu Ser His Ser Ala Lys Val Ser
197          565          570          575
199 cca gct gag cat gat atc caa att atg tct gac ctt cat gag cag agt 2433

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200	Pro	Ala	Glu	His	Asp	Ile	Gln	Ile	Met	Ser	Asp	Leu	His	Glu	Gln	Ser	
201			580					585					590				
203	cta	ccc	aag	aag	aaa	aag	aag	caa	aaa	ctt	gaa	gtg	act	cgt	gaa	aaa	2481
204	Leu	Pro	Lys	Lys	Lys	Lys	Lys	Gln	Lys	Leu	Glu	Val	Thr	Arg	Glu	Lys	
205			595					600					605				
207	cag	acc	atg	ata	gat	gac	atc	ccc	atg	gat	att	gtt	gaa	ctg	cta	gct	2529
208	Gln	Thr	Met	Ile	Asp	Asp	Ile	Pro	Met	Asp	Ile	Val	Glu	Leu	Leu	Ala	
209	610					615						620				625	
211	aaa	aac	cag	cat	gag	agg	cag	ctt	atg	act	gag	act	gat	tgt	tct	gac	2577
212	Lys	Asn	Gln	His	Glu	Arg	Gln	Leu	Met	Thr	Glu	Thr	Asp	Cys	Ser	Asp	
213						630						635				640	
215	atc	aac	cgt	att	caa	tcc	aag	aca	act	gct	gat	gat	gat	tgt	gta	ata	2625
216	Ile	Asn	Arg	Ile	Gln	Ser	Lys	Thr	Thr	Ala	Asp	Asp	Asp	Cys	Val	Ile	
217						645								655			
219	gta	gct	gcc	aag	gat	ggt	tca	gat	tat	gca	tca	agt	gtg	ttt	gac	act	2673
220	Val	Ala	Ala	Lys	Asp	Gly	Ser	Asp	Tyr	Ala	Ser	Ser	Val	Phe	Asp	Thr	
221						660								670			
223	aat	tcc	caa	cag	aag	tcc	ttg	gca	tcc	caa	agt	aca	cag	aag	gag	tta	2721
224	Asn	Ser	Gln	Gln	Lys	Ser	Leu	Ala	Ser	Gln	Ser	Thr	Gln	Lys	Glu	Leu	
225								680						685			
227	cag	ggt	cat	ttg	gca	ttg	acc	aca	caa	gag	tct	cca	cat	cct	cag	aac	2769
228	Gln	Gly	His	Leu	Ala	Leu	Thr	Thr	Gln	Glu	Ser	Pro	His	Pro	Gln	Asn	
229	690					695						700				705	
231	ttt	cag	tct	act	cag	gaa	cag	cag	aca	cat	ttg	cgg	atg	gaa	gaa	atg	2817
232	Phe	Gln	Ser	Thr	Gln	Glu	Gln	Gln	Thr	His	Leu	Arg	Met	Glu	Glu	Met	
233						710						715				720	
235	gtc	act	att	gct	gca	agc	tca	cca	cta	ttt	tca	cat	cat	gat	gat	cag	2865
236	Val	Thr	Ile	Ala	Ala	Ser	Ser	Pro	Leu	Phe	Ser	His	His	Asp	Asp	Gln	
237						725								735			
239	tat	att	gct	gaa	gca	cca	act	gaa	cat	tgg	ggc	cgt	aag	gac	gca	aag	2913
240	Tyr	Ile	Ala	Glu	Ala	Pro	Thr	Glu	His	Trp	Gly	Arg	Lys	Asp	Ala	Lys	
241						740								750			
243	aag	cta	acg	tgg	gag	caa	ttt	aag	gcc	act	aca	aga	aat	tct	cca	gca	2961
244	Lys	Leu	Thr	Trp	Glu	Gln	Phe	Lys	Ala	Thr	Thr	Arg	Asn	Ser	Pro	Ala	
245						755								765			
247	gca	aca	tgt	ggt	gct	caa	ttt	aga	cct	ggt	atc	caa	gca	gtt	gac	ttg	3009
248	Ala	Thr	Cys	Gly	Ala	Gln	Phe	Arg	Pro	Gly	Ile	Gln	Ala	Val	Asp	Leu	
249	770					775						780				785	
251	act	tct	act	cat	gtc	atg	gga	tct	tcc	agc	aat	tat	gca	tct	cgc	caa	3057
252	Thr	Ser	Thr	His	Val	Met	Gly	Ser	Ser	Ser	Asn	Tyr	Ala	Ser	Arg	Gln	
253						790										800	
255	cca	gta	att	gcg	cca	ctg	gac	cgc	tat	gct	gaa	aga	gcg	gtt	aac	cag	3105
256	Pro	Val	Ile	Ala	Pro	Leu	Asp	Arg	Tyr	Ala	Glu	Arg	Ala	Val	Asn	Gln	
257						805								815			
259	gtc	cat	gca	aga	aat	ttt	cca	agc	aca	tata	gca	acc	atg	gaa	gcg	agt	3153
260	Val	His	Ala	Arg	Asn	Phe	Pro	Ser	Thr	Ile	Ala	Thr	Met	Glu	Ala	Ser	
261						820								830			
263	aag	tta	tgt	gat	cgg	aga	aat	gct	gga	caa	gta	gtc	ttg	tat	cct	aaa	3201
264	Lys	Leu	Cys	Asp	Arg	Arg	Asn	Ala	Gly	Gln	Val	Val	Leu	Tyr	Pro	Lys	

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265      835      840      845
267 gaa tcc atg cct gcg acg cat ctt ctg aga atg atg gat cca tca aca 3249
268 Glu Ser Met Pro Ala Thr His Leu Leu Arg Met Met Asp Pro Ser Thr
269 850      855      860      865
271 tta gca agc ttc ccc aac tat gga act tct agc agg aac cag atg gag 3297
272 Leu Ala Ser Phe Pro Asn Tyr Gly Thr Ser Ser Arg Asn Gln Met Glu
273      870      875      880
275 tct caa ctt cat aat tct cag tat gca cat aat cag tac aaa gga tca 3345
276 Ser Gln Leu His Asn Ser Gln Tyr Ala His Asn Gln Tyr Lys Gly Ser
277      885      890      895
279 acc agc aca tca tat ggc agt aac ctg aat gga aag att cca ttg aca 3393
280 Thr Ser Thr Ser Tyr Gly Ser Asn Leu Asn Gly Lys Ile Pro Leu Thr
281      900      905      910
283 ttc gaa gac tta tca cgg cat cag ctg cat gat ctg cac aga cct tta 3441
284 Phe Glu Asp Leu Ser Arg His Gln Leu His Asp Leu His Arg Pro Leu
285      915      920      925
287 cgc cca cat cct aga gtt ggt gtg ctt ggc tcc ttg ctg cag aag gaa 3489
288 Arg Pro His Pro Arg Val Gly Val Leu Gly Ser Leu Leu Gln Lys Glu
289 930      935      940      945
291 att gca aac tgg tgc gag aac tgt ggc aca caa tct ggt tat aag tta 3537
292 Ile Ala Asn Trp Ser Glu Asn Cys Gly Thr Gln Ser Gly Tyr Lys Leu
293      950      955      960
295 gga gtg tca aca gga ata aca tgc cat cag atg aac aga aag gaa cat 3585
296 Gly Val Ser Thr Gly Ile Thr Ser His Gln Met Asn Arg Lys Glu His
297      965      970      975
299 ttt gaa gcc ctg aat tct gga atg ttt tca gca aaa tgg aat gca ttg 3633
300 Phe Glu Ala Leu Asn Ser Gly Met Phe Ser Ala Lys Trp Asn Ala Leu
301      980      985      990
303 cag ttg ggt tct gtt agc tcc agt gca gat ttt tta tca gcg agg aac 3681
304 Gln Leu Gly Ser Val Ser Ser Ser Ala Asp Phe Leu Ser Ala Arg Asn
305      995      1000      1005
307 agc ata gct caa tct tgg acc aga ggc aag ggt aaa atg gtt cat ccc 3729
308 Ser Ile Ala Gln Ser Trp Thr Arg Gly Lys Gly Lys Met Val His Pro
309 1010      1015      1020      1025
311 ttg gat cgg ttt gtg aga cag gat atc tgt ata act aac aag aac cca 3777
312 Leu Asp Arg Phe Val Arg Gln Asp Ile Cys Ile Thr Asn Lys Asn Pro
313      1030      1035      1040
315 gct gat ttt act aca atc agt aac gat aac gag tat atg gat tac cgc 3825
316 Ala Asp Phe Thr Thr Ile Ser Asn Asp Asn Glu Tyr Met Asp Tyr Arg
317      1045      1050      1055
319 tga agcagaaagt ggtgtgcata attcctgaac atttacaatc atacatttca 3878
322 tctttatggc gccaaatagt catactgtaa gaggagggt ttgctggatc tgctgtaagg 3938
324 cttcttgtaa gttgtggatg cccattttc tggatgggaa cctgccagac agtgaacaag 3998
326 ggctttgcaa ggtgcagcat ccggtttttg ttttgccagt ccaagaaacg tctcctgtt 4058
328 actttgtagt tgtactcata ctagtgcgtt tgtttgtaca aggagaaatg tgtaaccttg 4118
330 ttgaaaaaat gtctccccca ttttgttaatt accataagga ggtttatagt gttgtgagct 4178
332 gtgtgtgact gacggcgaga aatggttttg tcggtgttaa ggttgaaacg actagctctc 4238
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